Sequence-based investigation of MRSA Infection
Julie Segre (NHGRI) and researchers from NHGRI, CC, NIAID, and NCI

There are approximately 18,000 deaths in the U.S. each year from methicillin-resistant Staphylococcus aureus (MRSA) infections. Although MRSA was initially associated with hospitalization, community acquired MRSA has now emerged as a public health crisis. MRSA colonizes the nares of approximately 1.5% of healthy U.S. residents, who have a 23% annual risk of developing a MRSA infection. MRSA infections typically cause skin and soft tissue infection, but can also cause invasive infections such as pneumonia, bacteremia, and bone/joint infections. Co-morbidities of MRSA infection include diabetes, cancer, end-stage renal, and liver disease. We hypothesize that the transition between asymptomatic MRSA colonization and infection correlates with differences in the local microbial community structure and/or changes in the MRSA genome. The goals of this project are to (1) collect microbiome samples of atopic dermatitis and primary immunodeficiency Hyper-IgE patients and age-matched controls, who are both MRSA and non-MRSA carriers, (2) Establish the features of the microbial communities that are resident in these patients, and (3) Subject MRSA isolates to whole-genome sequencing and transcriptional profiling.